

RAW SEQUENCE LISTING

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Application Serial Number: 10/785, 220C
Source: IFW16
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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/785,220C

DATE: 12/28/2005

TIME: 13:17:34

Input Set : A:\39780-1216R1D4 saved November 17 2005.TXT
 Output Set: N:\CRF4\12282005\J785220C.raw

4 <110> APPLICANT: Ashkenazi, Avi J.
 5 Fong, Sherman
 6 Goddard, Audrey
 7 Gurney, Austin L.
 8 Napier, Mary A.
 9 Tumas, Daniel
 10 Wood, William I.
 12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
 13 THE TREATMENT OF DISEASES CHARACTERIZED BY A33- RELATED
 14 ANTIGENS
 16 <130> FILE REFERENCE: 39780-1216R1D4
 18 <140> CURRENT APPLICATION NUMBER: 10/785,220C
 19 <141> CURRENT FILING DATE: 2004-02-24
 21 <150> PRIOR APPLICATION NUMBER: US 09/254,465
 22 <151> PRIOR FILING DATE: 1999-03-05
 24 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
 25 <151> PRIOR FILING DATE: 1998-11-20
 27 <150> PRIOR APPLICATION NUMBER: US 60/066,364
 28 <151> PRIOR FILING DATE: 1997-11-21
 30 <150> PRIOR APPLICATION NUMBER: US 60/078,936
 31 <151> PRIOR FILING DATE: 1998-03-20
 33 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
 34 <151> PRIOR FILING DATE: 1998-09-17
 36 <160> NUMBER OF SEQ ID NOS: 30
 38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 40 <210> SEQ ID NO: 1
 41 <211> LENGTH: 299
 42 <212> TYPE: PRT
 43 <213> ORGANISM: Homo sapiens
 45 <400> SEQUENCE: 1
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 48 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 49 20 25 30
 50 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 51 35 40 45
 52 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 53 50 55 60
 54 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 55 65 70 75 80
 56 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 57 85 90 95
 58 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser

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59 100 105 110
 60 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 61 115 120 125
 62 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 63 130 135 140
 64 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 65 145 150 155 160
 66 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 67 165 170 175
 68 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 69 180 185 190
 70 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 71 195 200 205
 72 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 73 210 215 220
 74 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 75 225 230 235 240
 76 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 77 245 250 255
 78 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 79 260 265 270
 80 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 81 275 280 285
 82 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 83 290 295
 86 <210> SEQ ID NO: 2
 87 <211> LENGTH: 321
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Homo sapiens
 91 <400> SEQUENCE: 2
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 93 1 5 10 15
 94 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
 95 20 25 30
 96 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
 97 35 40 45
 98 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
 99 50 55 60
 100 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
 101 65 70 75 80
 102 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
 103 85 90 95
 104 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
 105 100 105 110
 106 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
 107 115 120 125
 108 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
 109 130 135 140
 110 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg

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111 145 150 155 160
112 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
113 165 170 175
114 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
115 180 185 190
116 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
117 195 200 205
118 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
119 210 215 220
120 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
121 225 230 235 240
122 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
123 245 250 255
124 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
125 260 265 270
126 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
127 275 280 285
128 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
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131 305 310 315 320
132 Arg
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137 <211> LENGTH: 390
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Consensus DNA Sequence
144 <400> SEQUENCE: 3
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146 ttgtatggtc tctgaggaag gcggcaacag ctatggggag gtcaaggctca agctcatcg 120
147 gcttgcct ccattccaagc ctacagttaa catccccctcc tctgcccacca ttgggaaccg 180
148 ggcagtgctg acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
149 agatggata gtgatgccta cgaatcccaa aagcaccctg gccttcagca actcttccta 300
150 tgtcctgaat cccacaacag gagagctggt ctttgcattt ctgtcagcct ctgataactgg 360
151 agaatacagc tgtgaggcac ggaatggta 390
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 726
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Consensus DNA Sequence
161 <400> SEQUENCE: 4
162 tctcagtccc ctcgtgttag tcgcggagct gtgttctgtt tcccaggagt cttcggcgg 60
163 ctgttgcct caggtgcgtc tgatcgcgt ggggacaaag gcgcaagctc gagagggaaac 120
164 tggcgtgcct cttcatattt ggcgtccctgt tgtgtccctt ggcattggc agtgttacag 180
165 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
166 gcctactcgg gctttcttc tccccgtgt gagtgaaat ttgaccaagg agacaccacc 300
167 agactcggtt gctataataa caagatcaca gcttcctatg aggaccgggt gaccccttg 360

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168 ccaactggta tcaccccaa gtccgtgaca cgggaagaca ctgggacata cacttgtatg 420
 169 gtctctgagg aaggccgcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttgc 480
 170 cctccatcca agcctacagt taacatcccc tcctctgcca ccattggaa cgggcagtg 540
 171 ctgacatgct cagaacaaga tggttcccca ccttctgaat acacctgtt caaagatggg 600
 172 atagtatgc ctacgaatcc caaaagcacc cgtgccttca gcaactttc ctatgtcctg 660
 173 aatccccaaa caggagagct ggtcttgat cccctgtcag cctctgatac tggagaatac 720
 174 agctgt 726
 176 <210> SEQ ID NO: 5
 177 <211> LENGTH: 1503
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Artificial Sequence
 181 <220> FEATURE:
 182 <223> OTHER INFORMATION: Consensus DNA Sequence
 184 <400> SEQUENCE: 5
 185 gcaggccaaag taccaggggcc gcctgcattt gaggccacaag gttccaggag atgtatccct 60
 186 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120
 187 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaaact 180
 188 ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
 189 aatgaggatt agcctcaat gccagggttc ggggttctcc tcccatcaat tatatttgg 300
 190 ataagcaaca gactaataac cagggaaaccc atcaaaggtag caaccctaag taccttactc 360
 191 ttcaagcctg cggtgatagc cgactcaggc tcctatttct gcactgccaa gggccagg 420
 192 ggctctgagc agcacagcga cattgtgaag tttgtggta aagactcctc aaagctactc 480
 193 aagaccaaga ctgaggcacc tacaaccatg acataaccct tgaaagcaac atctacagt 540
 194 aagcagtccct gggactggac cactgacatg gatggctacc ttggagagac cagtgcctgg 600
 195 ccaggaaaga gcctgcctgt ctttgcacat atcctcatca tctccttgc ctgtatgg 660
 196 gtttttacca tggctatat catgctctgt cggaaagacat cccaaacaaga gcatgtctac 720
 197 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaccat gagggtg 780
 198 atcttcgcaa gtggctgctc cagtgtatg ccaacttccc agaatctgg gcaacaacta 840
 199 ctctgtatgag ccctgcatag gacaggagta ccagatcatc gcccagatca atggcaacta 900
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 203 ctaccaacac tggagccgct gggagtcact ggcttgcct tggaaattgc cagatgcata 1140
 204 tcaagtaagc cagctgtgg atttggctct gggcccttct agtatctctg ccgggggctt 1200
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 206 tgcctacaga cactattcaa ctttgcacat ttgcaccag aagaccggag gggaggctca 1320
 207 gctctgccag ctcagaggac cagctatatac caggatcatt tctcttctt cagggccaga 1380
 208 cagttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
 209 agtctaattgt tctgactctc tcctgggtct caataaaat ctaatcataa cagcaaaaaaa 1500
 210 aaa 1503
 212 <210> SEQ ID NO: 6
 213 <211> LENGTH: 319
 214 <212> TYPE: PRT
 215 <213> ORGANISM: Homo sapiens
 217 <400> SEQUENCE: 6
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 220 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
 221 20 25 30

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222 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
 223 35 40 45
 224 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
 225 50 55 60
 226 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
 227 65 70 75 80
 228 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
 229 85 90 95
 230 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
 231 100 105 110
 232 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
 233 115 120 125
 234 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
 235 130 135 140
 236 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
 237 145 150 155 160
 238 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
 239 165 170 175
 240 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
 241 180 185 190
 242 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
 243 195 200 205
 244 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
 245 210 215 220
 246 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
 247 225 230 235 240
 248 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
 249 245 250 255
 250 Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
 251 260 265 270
 252 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
 253 275 280 285
 254 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
 255 290 295 300
 256 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
 257 305 310 315
 260 <210> SEQ ID NO: 7
 261 <211> LENGTH: 2181
 262 <212> TYPE: DNA
 263 <213> ORGANISM: Homo sapiens
 265 <400> SEQUENCE: 7
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 267 tttgagcctc tttggtagca ggaggctgga agaaaaggaca gaagtagctc tggctgtgat 120
 268 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
 269 catcctggaa gtgcacagaga gtgtAACAGG accttggaaa ggggatgtga atttccctg 240
 270 cacctatgac cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
 271 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
 272 gtaccagggc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaaattgag 420
 273 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480

VERIFICATION SUMMARY

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